

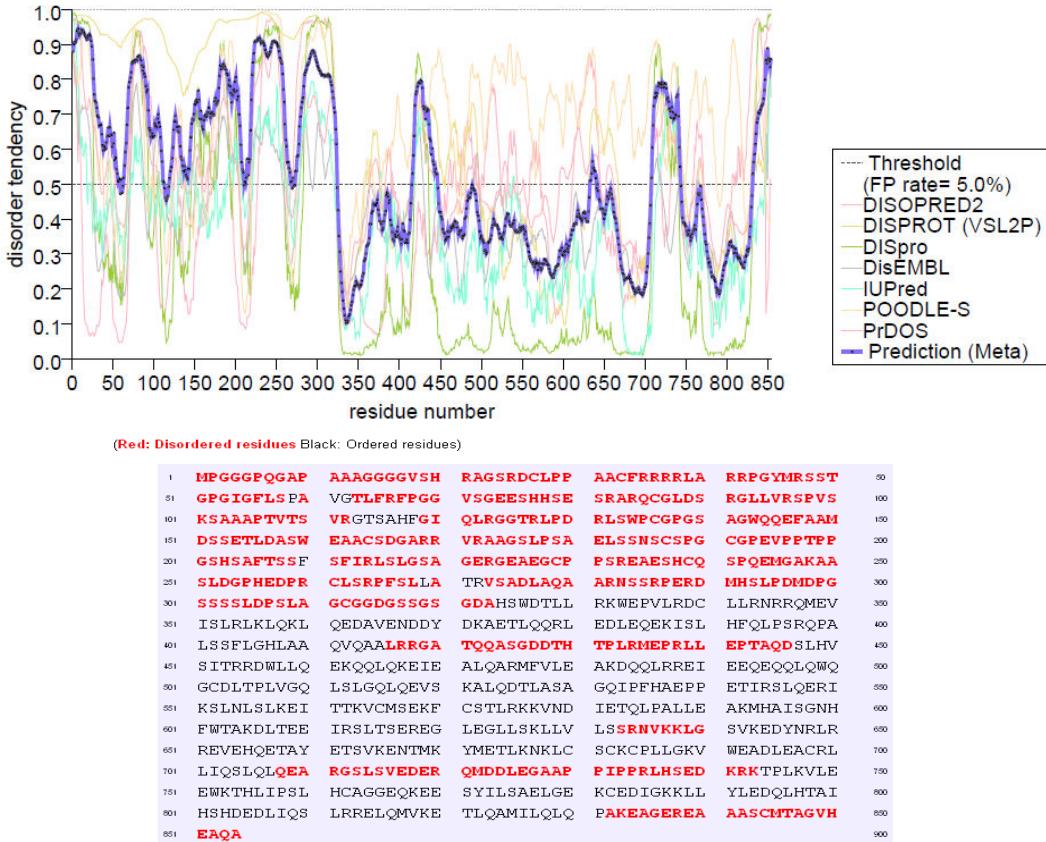
Supplementary information

DISC1: structure, function and therapeutic potential for major mental illness

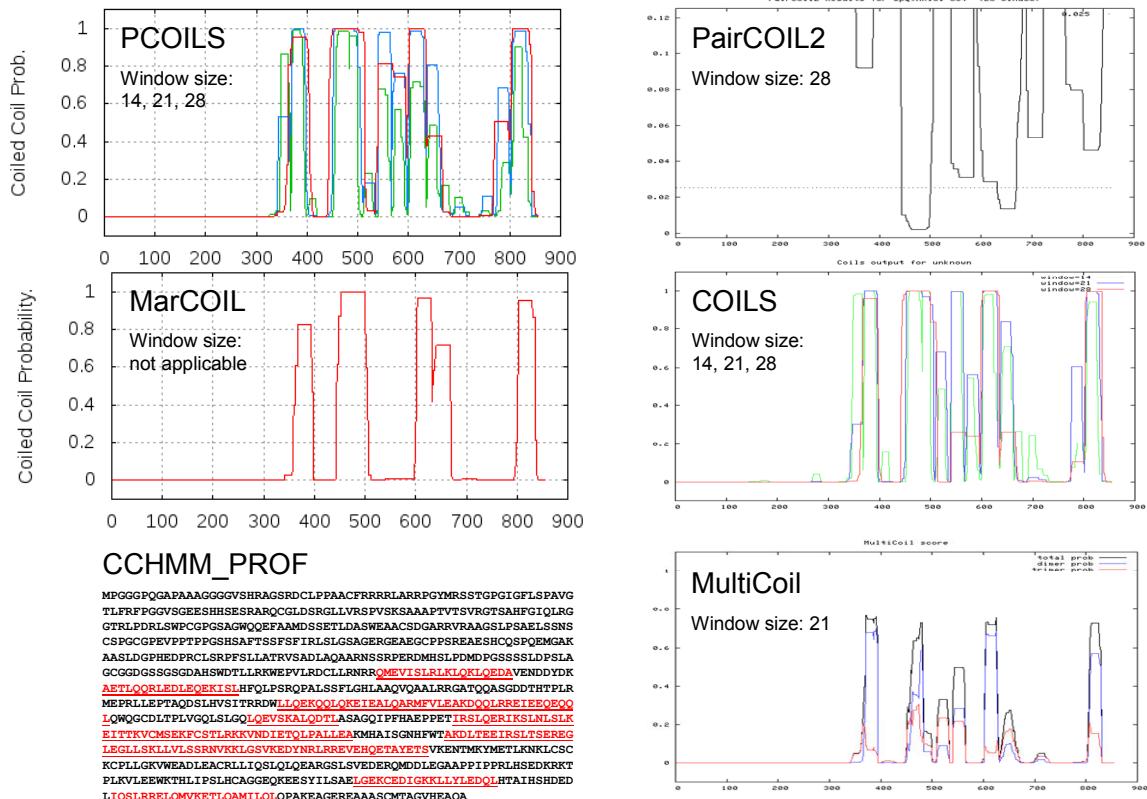
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Supplementary Figure 1: MetaPrDOS prediction of disorder in DISC1 using a 5% false positive rate threshold. MetaPrDOS (1) provides an integrated consensus disorder prediction (blue with dots) derived from seven independent disorder prediction methods. The individual prediction assignment for each method (refer to key above) is also shown. From the derived consensus disorder prediction, using a 5% false positive rate estimate threshold (the default setting) almost the entire N terminus - ~89% (310 out of 350 residues) - is predicted to be disordered



Supplementary Figure 2: Broad consensus of coiled coil prediction from all methods. Application of six coiled coil prediction programs on the DISC1 sequence: CCHMM_PROF (2), COILS (3), MarCoil (4), Multicoil (5), PairCoil2 (6) and PCOILS (7). The window size used in each case is shown (where applicable). All six programs predict coiled coil regions within the C terminus by broad consensus. For CCHMM_PROF, the coiled coil boundaries shown (red) are as follows: 347-364, 373-390, 458-497, 516-527, 543-591, 604-663, 778-796 and 808-829. For the other programs, the residue number is plotted along the x-axis, while the coiled-coil propensity is plotted along the y-axis.

Region on DISC1	Yeast 2-hybrid DISC1-Interactor	Reference
1-597, not 598-854	Citron	(8)
598-854, not 1-597	Dynactin, spectrin, 14-3-3 γ , KCNQ5	(8)
1-854, not 1-597	ACTG1, AGTPBP1, AKAP9, ARIH2M, BICD1, C2ORF4, C14ORF135, C22ORF1, CDC5L, CDK5RAP3, CRNL1, DMDEXOCT, DPYSL2, DPYSL3, EEF2, FBXO41, FLJ13386, FLJ22386, GNB1, GRASP2, KIAA0470, KIAA0826, KIFAP3, MATR3, MN7, MYT1L, OLFM1, PGK1M, PPM1E, PPPR41, RABGAP1, RAD21, SH3BP5, SMARCE1, SNX6, SPTAN1, TIAM2, TNKS, TUBB, TUBB2, XPNPEP1, XRN2, ZNF197	(9)
1-597, not 1-854	C6ORF182, C14ORF166, DCTN1, DKFZP434G156, MGC4170, MGC45441, PPP5C, SMC2L1, SPARCL1, SRGAP2, ST18, UTRN, YWHAQ, YWHAZ	(9)
1-597 and 1-854	CLU, DCTN2, DNAJC7, DNCH1, DST, KIF3A, KIF3C, MACF1, NUP160, SEC3L1, SPTBN1, TFIP11, TRAF3IP1, YWHAE	(9)

Supplementary Table 1: Interaction regions mapped by yeast 2-hybrid (Y2H) experiments only. Note these are not the total number of DISC1-interactors known by Y2H, but only those for which DISC1 construct regions have been identified as binding regions. All gene or protein names as reported in original publications.

References

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